

Figure 1A

1 CAAGCACTGTGCTAAAGTGTTCATATGTCATGAAAAGTTGTGCCAGAAAAATTATGGT 60

61 TTGAACATGGGCAGTTTCTCCTACCGTCAGCTATATCCACAAGCATCACATGAAGTGA 120

121 GATCTGGCAGCTCTGTGTATTTTCAGTCAAGTTCACAATGAAACCTGACAATAATGGTAA 180

181 AAACCAATACGGACATCTGAGTAACTGGGGAATTGGCCTGCCTTGCATGTGAGCTTGATG 240

241 GAAGATTGGATATAGACGAGTTGATTATATTTTATGAAGTAGCAGCTCACTACCATCCAC 300

301 CATCCAGGGTTTAAACTACTTTTTCAGCATCACTTCACCTGTGGACTCTTATACATTTTG 360

361 ATTTCTTGGGGGAAAAATACTGGGATAAGAGGAGGTCATTTTAAATAAGTTAGCATCCT 420

421 TTTCCCTTTCTTACAAGTTGATCCAAAGGATAAGGCTGTGACTCCATTGGATTGCACCTT 480

481 TAAATCAAAATAGCAGCAGCAGAAGAAAGGGACAATGGCTCTGAGTGAAACTGTAGTCG 540

1 M A L S G N C S R 9

541 TTATTATCCTCGAGAACAAGGGTCCGCAGTTCCCAACTCCTTCCCTGAGGTGGTAGAGCT 600

10 Y Y P R E Q G S A V P N S F P E V V E L 29

601 GAATGTCGGGGTCAAGTTTATTTTACTCGCCATTCCACATTGATAAGCATCCCTCATTC 660

30 N V G G Q V Y F T R H S T L I S I P H S 49

661 CCTCCTGTGGAATGTTTCCCCAAAGAGACACGGCTAATGATCTAGCCAAGGACTC 720

50 L L W K M F S P K R D T A N D L A K D S 69

721 CAAGGGAAGGTTTTCATTGACAGAGATGGATTCTTGTTCGGTTATATTCTGGACTATCT 780

70 K G R F F I D R D G F L F R Y I L D Y L 89

781 CAGGGACAGGCAGGTGGTCCTGCCTGATCACTTTCCAGAAAAAGGAAGACTGAAAAGGGA 840

90 R D R Q V V L P D H F P E K G R L K R E 109

841 AGCTGAATACTTCCAGCTCCCAGACTTGGTCAAACCTCCTGACCCCGATGAAATCAAGCA 900

110 A E Y F Q L P D L V K L L T P D E I K Q 129

901 AAGCCCAGATGAATTCTGCCACAGTGACTTTGAAGATGCCTCCCAAGGAAGCGACACAAG 960

130 S P D E F C H S D F E D A S Q G S D T R 149

961 AATCTGCCCCCTTCCCTCCCTGCTCCCTGCCGACCGCAAGTGGGGTTTCATTACTGTGGG 1020

150 I C P P S S L L P A D R K W G F I T V G 169

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Figure 1B

1021 TTACAGAGGATCCTGCACCTTGGGCAGAGAGGGACAGGCAGATGCCAAGTTTCGGAGAGT 1080
 170 Y R G S C T L G R E G Q A D A K F R R V 189

1081 TCCCCGATTTTGGTTTGTGGAAGGATTTCCCTTGGCAAAAGAAGTCTTTGGAGAACTTT 1140
 190 P R I L V C G R I S L A K E V F G E T L 209

1141 GAATGAAAGCAGAGACCCTGATCGAGCCCCAGAAAGATACACCTCCAGATTTTATCTCAA 1200
 210 N E S R D P D R A P E R Y T S R F Y L K 229

1201 ATTCAAGCACCTGGAAAGGGCTTTTGATATGTTGTCAGAGTGTGGATTCCACATGGTGGC 1260
 230 F K H L E R A F D M L S E C G F H M V A 249

1261 CTGTAACCTCATCGGTGACAGCATCTTTCATCAACCAATATACAGATGACAAGATCTGGTC 1320
 250 C N S S V T A S F I N Q Y T D D K I W S 269

1321 AAGCTACACTGAATATGTCTTCTACCGTGAGCCTTCCAGATGGTCACCCTCACACTGCGA 1380
 270 S Y T E Y V F Y R E P S R W S P S H C D 289

1381 TTGCTGCTGCAAGAATGGCAAAGGTGACAAAGAAGGGGAGAGCGGCACGTCTTGCAATGA 1440
 290 C C C K N G K G D K E G E S G T S C N D 309

1441 CCTCTCCACATCTAGCTGCGACAGCCAGTCTGAGGCCAGCTCTCCCCAGGAGACGGTCAT 1500
 310 L S T S S C D S Q S E A S S P Q E T V I 329

1501 CTGTGGTCCCGTGACACGCCAGACCAACATCCAGACTCTGGACCGTCCCATCAAGAAGGG 1560
 330 C G P V T R Q T N I Q T L D R P I K K G 349

1561 CCCTGTCCAGCTGATCCAACAGTCAGAGATGCGGCGGAAAAGCGACTTACTCCGGATTCT 1620
 350 P V Q L I Q Q S E M R R K S D L L R I L 369

1621 GACTTCAGGCTCCAGGGAATCGAACATGAGCAGCAAAAAAAGCTGTTAAAGAAAAGCT 1680
 370 T S G S R E S N M S S K K K A V K E K L 389

1681 CTCAATTGAGGAGGAGCTGGAGAAATGTATCCAGGATTTCTAAAAAATAATCCAGA 1740
 390 S I E E E L E K C I Q D F L K K K I P D 409

1741 TCGGTTTCTGAGAGAAAACATCCTTGGCAATCTGAACTTTTAAGGAAGTATCATCTATA 1800
 410 R F P E R K H P W Q S E L L R K Y H L 428

1801 AGGGAGGGCTGGGGGCGGGGAAAAAAAAAAAAAGAGTCATTTTGAAATTAACCTCATAA 1860

1861 AAGGAATTCATATTTTAAAGGAAAAAATACAATAATGATGCACATTTCTTAGAACACA 1920

1921 ATAGTCCATTGATATACTACTGCCTACTTTACCTAGTTCACCTTAACATGTAAATCCACA 1980

Figure 1C

1981 GGGTAGATTTCTTTCTAGATGTGGAAGTACAAGAAAATCTTTTTTAGTTATTTGTTTGT 2040

2041 TACTTCGTCCCATGTGCTAACTATCTTATATATAATGAGAGCCAGCTACGTAAAAGTAGC 2100

2101 TGAGAGGCCTTGGGAGTCATTTATCCCAAAC TGGGTTTTTCTCTCATCCTTCTACCTCC 2160

2161 CTCCTTTGAATGAGGGTATGGTAGAAAAAGATCTGGCCCAATGGCATAAGTTTGGAATTT 2220

2221 TTAATTTTGGTTTTTTCCTTTTGT TTTATGGGGTTGGGGGAATGGCAGATTTATATGACTT 2280

2281 TTCACTCAAATCTATATGTGCCAGTTTATATTGACTCCGTATGCATGAGTATTTGTGCAA 2340

2341 CACAAGCACAACTAAGTATGTATATACACATGACGCACACGATGCCAGGGCCTAGACCTC 2400

2401 CCAAGGGCTGTGCTCCTGCTCCAGCAGCCCTCTCTTAGAATATTTTCAGATGGATGAGCT 2460

2461 TCTGACTCTTTCTTAAATCTTTTGGGAAGATTTCCAGCCTTTCTTCACAACACTTTC 2520

2521 TAACATCAAATGACTCTCATCATCAACAAATGTATTCCTTATTGTGAAATTAATACCTT 2580

2581 CAGGCTCCATTTTACTGCTTTGCTCTTTGTCTGCATTAAGAGAGGATGAGGAGAGCTGGT 2640

2641 CAAACATTCCTTGTGTTAAAAAATCAAACATTCATATCCACAAAATTTTCTGCTAAATG 2700

2701 ACTCCACACTCAGCCTTCTCTACCCTGAACTGAATTATCACCCCTTTTCTCCATGTTTTCA 2760

2761 GAGTCTTACTGCCCACAGTTTAATGGTGTGGCCTTTCCACATAATCCACATTAAGTTCT 2820

2821 GTGTTCCCTGTGTTGTTGTGGAAC TAAGGACAACACACAGTACTTGAATAAGGGTCCGGCC 2880

2881 TTTTGTTTGT TTTTAGAGAAAGTTGTATTCCACACACAACCTAATAATTTCTTATAAAAAT 2940

2941 TTTAAACTACAAAGCTACATTTTACTTGCTTGTAGCCGTTTTTGT TGCCTTTGGGATT 3000

3001 CGGGCTTTGGCTGTGCCCATGCTAGGATTTAGCTGTGTCATTTTTATGATGTCTGTAACA 3060

3061 ACCCAACAAGGTAAC TGAAGCTCCAGAGTTAAGGTTTCAGATTTCTAAATGAACTATCT 3120

3121 TTTTCAATTACATCCTGACTTGTATAGACACAGCCAAAAAGAACTGTTAATAGCCATCC 3180

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20476.4895007

Figure 1D

3181 GTCCATGTA·ACTCTGTATTTT·ACTAAGGT·ACCAATAGCTCTTTCATAGACTTGTGCTACA· 3240
3241 AGAAGGTTAA·AGACCAGTTT·TTATTTTCAGCATTCCTCATGCATTCAGTGGTAACCAAA· 3300
3301 AAATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTTATTGCGTGTG· 3360
3361 TGTGCATGTGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATGATTAAAAAAAAAAAA· 3420
3421 AAA 3468

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Figure 2A

1			50
K+betaM2	(1)	-----MALSGNCSRYYPREQGSAVPNSIP	VELNVGCGVYFTRHSTLIS
AAF558201	(1)	-----	MPETLELVGCVSYTTLATILLO
CAA20329.1	(1)	-----	MTSVEDVITLVNVCCTMYTTRSTLISK
Y34129	(1)	-----	MDNGDWGYMTTPVTLNVGCHVYTTSLTTLTK
Y34125	(1)	MSRPLITRSPASPLXNQGIPTPAQLTKSNAPVH	LVGCHVYTTSSLATLTK
		51	100
K+betaM2	(46)	IPHSLLWKMFPSP--KRDTANDLAKDSKGRF	IDRDGFLERYITLDYLRDRQ
AAF558201	(24)	DKSTLLAEELFG----EGRDSLAKDSKGRYF	IDRDGVLERYITLDYLRDKA
CAA20329.1	(27)	ETDILLANIASGSLSEDEQANVTLPDGTF	VDRDGPLEAYVLFHFLRTDK
Y34129	(33)	YPDSMLCAMFGG----D--FPDARDPQGNV	VDRDGPLERYVLFNFLTSE
Y34125	(51)	YPESRLGRIFDG----T-EPIVLDSLQHYF	VDRDGOMERYILNFLTSTK
		101	150
K+betaM2	(94)	VVLPHHFPEKGRLEKEAEYFQLPDLV	KLLTPDIKQSPDEFCHSDFEDAS
AAF558201	(69)	LHLPEGFRERQRLLREARHFKLTAM	ECIRSEIDAR-----
CAA20329.1	(77)	LSLPQOFREVARLKDEADFYLERHSTLLSNASSIS	-PRPR-----
Y34129	(77)	LTLPLDFKEFDLLREADFYQLEPLIQCLNDPKPLY	-----
Y34125	(96)	LLLPDFFQDYTLIYEAKYFQLQPM	LEMERWKQDR-----
		151	200
K+betaM2	(144)	QGS DTRICPPSSLLPADRKWGFITV	GYRGSCTLGRHQADAKFRFVPRIL
AAF558201	(105)	-----	PP----GCITLGYRGSFQFGKGLADVKFRKLSRIL
CAA20329.1	(117)	-----	TANGYNTITSCAETGGYITLGYRGTFAFGRDQADVKFRKLHRIL
Y34129	(113)	-----	PMDTFEEVVELSSTRKLSKYSNPVAVITITLITTK
Y34125	(132)	-----	ETGRFSRPCECLVVRVAPDLGERITLGGDKSLIEEVF
		201	250
K+betaM2	(194)	VCGRISLAKEVFGETLINESRDPDR-AP	RYTSRFYLLKFKILERAFFDMLSE
AAF558201	(137)	VCGRVAQCREVFCDTLINESRDPDHGGT	DRYTSRFFLLKHCYIEQAFDNLHD
CAA20329.1	(162)	VCGRATLCREVFADTLINESRDPGG--	PDGE-----
Y34129	(149)	VHSLLEGISNYFTWVWKHMDLRD---	CQVSFTFGPCDYHQEVSLRVHLM
Y34125	(169)	PEIGDVMCNIVNAGWNHISTIVIR----	FPLNGYCHLNSVQVLERLQQ
		251	300
K+betaM2	(243)	CGPHMVACNSSVTASFIN----	QYTDDKIWSSYTEYVFYREPSRWSPSH
AAF558201	(187)	HGYRMAGSCGSGTAGSAAEPKPGVDTE	ENRWNHYNEFVFIRD-----
CAA20329.1	(191)	-----	-----
Y34129	(196)	EYITKQGFTIRNTRVHHMSE	RANENTVPHNWTFCRLARKTDD-----
Y34125	(213)	RGEELVGCSCGGVDSSQFSEYVLRREL	RTRTPRVPSVIRIKQEPLE-----
		301	350
K+betaM2	(288)	CDCCCKNGKGDKEGESGTSCNDLSTSS	CDSQSEASSPQETVICGPVTRQT
AAF558201	(229)	-----	-----
CAA20329.1	(191)	-----	-----
Y34129	(238)	-----	-----
Y34125	(257)	-----	-----
		351	400
K+betaM2	(338)	NIQTLDRPIKKGVPVQLIQQSEMRRKSD	LLRILTSGSRESNMSSKKKAVKE
AAF558201	(229)	-----	-----
CAA20329.1	(191)	-----	-----
Y34129	(238)	-----	-----
Y34125	(257)	-----	-----

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Figure 2B

		401	441
K+betaM2	(388)	KLSIEEELEKCIQDFLKKKIPDRFPERKHPWQSELLRKYHL	
AAF558201	(229)	-----	
CAA20329.1	(191)	-----	
Y34129	(238)	-----	
Y34125	(257)	-----	
Consensus	(401)		

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Figure 3

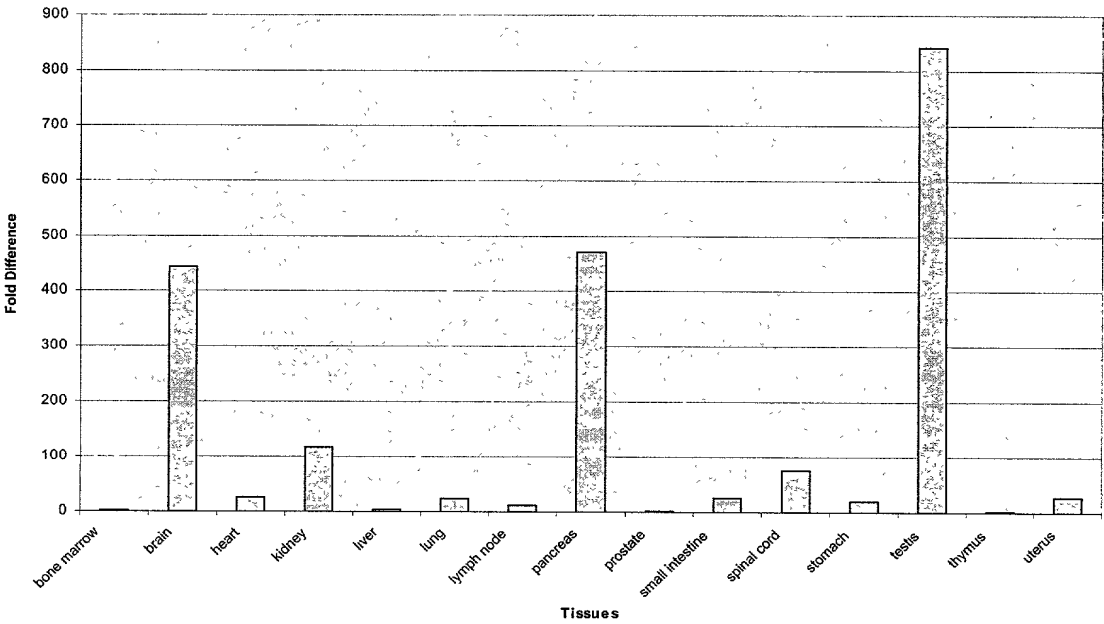


Figure 4.

Protein	Genbank ID	Identities	Similarities
Human potassium channel K+Hnov28	gi Y34129	31%	41%
Drosophila CG10830 protein	gi AAF55820.1	52%	66%
Caenorhabditis K+ channel tetramerisation domain	gi CAA20329.1	42%	51%
Human potassium channel K+Hnov27	gi Y34125	32%	41%

Figure 5

